

SEQUENCE LISTING

<110> Viaxxel Biotech GmbH

<120> Compounds that affect CD83 expression, pharmaceutical compositions comprising said compounds and methods for identifying said compounds

<130> 84201

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
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35	40	45	
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gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt	240		
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly			
65	70	75	80
tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac	288		
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn			
85	90	95	
act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg	336		
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro			
100	105	110	
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Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly			
115	120	125	
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Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
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Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct	528		
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165	170	175	
aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag	576		
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Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
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Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu

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130              135              140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
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Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
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Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
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Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
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Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
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tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac 337
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Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
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Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
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Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
160 165 170

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Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
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Thr Leu Pro Lys Thr Glu Thr Val

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Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
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 115 120 125

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 130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
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Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
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Thr Glu Thr Val
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 165 170 175

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 180 185 190

gtg gca ctc ctc tcg cag ctg tac cac tcg cca gcg cga cgg ttc gga 624
 Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly
 195 200 205

ggc ccc gtt cac cac cag gcg cag aga ttc agg ttc tcc ccc atg ggc 672
 Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly
 210 215 220

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 225 230 235 240

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 245 250 255

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 275 280 285

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10025367-121901
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Thr Asn Lys Ser His Lys

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35 40 45

Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly

50 55 60

Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr

65 70 75 80

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ggc cca acc acc ata aac aac aac tgt tcg tca cca gtt gac tct ggg 96

Gly Pro Thr Thr Ile Asn Asn Asn Cys Ser Ser Pro Val Asp Ser Gly

20 25 30

aac aca gaa gac agc aag acc aac tta ata gtc aac tac ctt cct cag 144

Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln

35 40 45

aac atg aca cag gag gaa cta aag agt ctc ttt ggg agc att ggt gaa 192

Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu

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Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu

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Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala

85 90 95

atc aac acc ctg aat gga ttg aga ctt caa acc aaa aca ata aaa gtt 336

Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val

100 105 110

tcc tat gct cgc cca agt tca gct tct atc aga gat gca aat tta tat 384

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr

115 120 125

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130 135 140

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Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp
225 230 235 240

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260 265 270

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Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln
 35 40 45

Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu
 50 55 60

Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu
 65 70 75 80

Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala
 85 90 95

Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val
 100 105 110

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr
 115 120 125

Val Ser Gly Leu Pro Lys Thr Met Thr Gln Lys Glu Leu Glu Gln Leu
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 145 150 155 160

Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg
 165 170 175

Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro
 180 185 190

Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln
 195 200 205

Lys Thr Asn Gln Ala Ile Leu Ser Gln Leu Tyr Gln Ser Pro Asn Arg
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Pro Ala Gly Pro Ala Leu Pro Asn Gly Pro Leu Leu Gly Thr Asn Gly

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atc aac acc ctc aac ggc ctc aaa tta cag acg aag acc atc aag gtg 336

Ile Asn Thr Leu Asn Gly Leu Lys Leu Gln Thr Lys Thr Ile Lys Val

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gtc agc ggg ctc ccc aag acc atg agc cag aaa gag atg gag cag ctc 432

Val Ser Gly Leu Pro Lys Thr Met Ser Gln Lys Glu Met Glu Gln Leu

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Ala	Gly	Gly	Trp	Cys	Ile	Phe	Val	Tyr	Asn	Leu	Ser	Pro	Glu	Ala	Asp	
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Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe Gly Ala Val Thr Asn
 290 295 300

gtc aag gtc atc cgt gat ttc acc acc aac aag tgc aag ggt ttc ggc 960
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 305 310 315 320

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 Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser
 325 330 335

ctg aac ggc tat cgc ctg gcc gag cgc gtg ctg cag gtc tcc ttc aag 1056
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 340 345 350

acc agc aaa cag cac aag gcg 1077
 Thr Ser Lys Gln His Lys Ala
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<213> Homo sapiens

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Ala Thr Asp Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln
 35 40 45

Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp
 50 55 60

1005367 44400

Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Ile Ala
245 250 255

Ile Asp Gly Met Ser Gly Leu Ala Gly Val Gly Leu Ser Gly Gly Ala
 260 265 270

Ala Gly Gly Trp Cys Ile Phe Val Tyr Asn Leu Ser Pro Glu Ala Asp
 275 280 285

Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe Gly Ala Val Thr Asn
 290 295 300

Val Lys Val Ile Arg Asp Phe Thr Thr Asn Lys Cys Lys Gly Phe Gly
 305 310 315 320

Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser
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Leu Asn Gly Tyr Arg Leu Ala Glu Arg Val Leu Gln Val Ser Phe Lys
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Thr Ser Lys Gln His Lys Ala
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10

15

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Thr Ser Asn Thr Ser Asn Gly Pro Ser Ser Asn Asn Arg Asn Cys Pro	
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tct ccc atg caa aca ggg gca acc aca gat gac agc aaa acc aac ctc	144
Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu	
35 40 45	
atc gtc aac tat tta ccc cag aat atg acc caa gaa gaa ttc agg agt	192
Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser	
50 55 60	
ctc ttc ggg agc att ggt gaa ata gaa tcc tgc aaa ctt gtg aga gac	240
Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp	
65 70 75 80	
aaa att aca gga cag agt tta ggg tat gga ttt gtt aac tat att gat	288
Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp	
85 90 95	
cca aag gat gca gag aaa gcc atc aac act tta aat gga ctc aga ctc	336
Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu	
100 105 110	
cag acc aaa acc ata aag gtc tca tat gcc cgt ccg agc tct gcc tca	384
Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser	
115 120 125	
atc agg gat gct aac ctc tat gtt agc ggc ctt ccc aaa acc atg acc	432
Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr	
130 135 140	
cag aag gaa ctg gag caa ctt ttc tcg caa tac ggc cgt atc atc acc	480
Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr	
145 150 155 160	
tca cga atc ctg gtt gat caa gtc aca gga gtg tcc aga ggg gtg gga	528

165 170 175

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly

180 185 190

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys

195 200 205

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln

210 215 220

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln

225 230 235 240

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val

245 250 255

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

260 265 270

Phe Ser Pro Ile Thr Ile Asp Gly Met Thr Ser Leu Val Gly Met Asn

275 280 285

Ile Pro Gly His Thr Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu

290 295 300

Ser Pro Asp Ser Asp Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe

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              325              330              335

tgc aag gga ttc ggc ttt gtc acc atg acc aac tat gat gag gcg gcc      1056
Cys Lys Gly Phe Gly Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala
              340              345              350

atg gcc atc gcc agc ctc aac ggg tac cgc ctg gga gac aga gtg ttg      1104
Met Ala Ile Ala Ser Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu
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caa gtt tcc ttt aaa acc aac aaa gcc cac aag tcc                        1140
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Thr Ser Asn Thr Ser Asn Gly Pro Ser Ser Asn Asn Arg Asn Cys Pro
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Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu
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Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser
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Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp
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Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp
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Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu
100 105 110

Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser
115 120 125

Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr
130 135 140

Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr
145 150 155 160

Ser Arg Ile Leu Val Asp Gln Val Thr Gly Val Ser Arg Gly Val Gly
165 170 175

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly
180 185 190

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys
195 200 205

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln
210 215 220

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln
225 230 235 240

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val
245 250 255

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

10015357 121901

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260
265
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Ile Pro Gly His Thr Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu
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Ser Pro Asp Ser Asp Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe
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Gly Ala Val Asn Asn Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys
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330
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Cys Lys Gly Phe Gly Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala
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345
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Met Ala Ile Ala Ser Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu
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365

Gln Val Ser Phe Lys Thr Asn Lys Ala His Lys Ser
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380

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